STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/576,439_
Source: _1EwP_
Date Processed by STIC: _5/1/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/576,439_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5__∪__Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s)_____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s)_____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s)____ missing the <220> "Feature" and associated numeric identifiers and responses. Use
of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – STIC Systems Branch – 03/02/06

IFWP

RAW SEQUENCE LISTING   DATE: 05/01/2006
PATENT APPLICATION: US/10/576,439   TIME: 09:45:10

Input Set : A:\Seq.ST25.txt
Output Set: N:\CRF4\05012006\J576439.raw

```
 3 <110> APPLICANT: Theratechnologies Inc.
 4       Lussier, Bruno
 5       Vachon, Luc
 6       Allas, Soraya
 7       Abribat, Thierry
 9 <120> TITLE OF INVENTION: Selection and treatment of patients suffering from wasting
11 <130> FILE REFERENCE: 09555.0151USWO
13 <140> CURRENT APPLICATION NUMBER: US/10/576,439
14 <141> CURRENT FILING DATE: 2006-04-20
17 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001843
18 <151> PRIOR FILING DATE: 2004-10-20
20 <150> PRIOR APPLICATION NUMBER: 60/512,198
21 <151> PRIOR FILING DATE: 2003-10-20
23 <160> NUMBER OF SEQ ID NOS: 7
25 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 30
29 <212> TYPE: PRT
30 <213> ORGANISM: Artificial sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: GRF peptide
36 <220> FEATURE:
37 <221> NAME/KEY: VARIANT
38 <222> LOCATION: (1)..(1)
39 <223> OTHER INFORMATION: Xaa = Tyr or His
41 <220> FEATURE:
42 <221> NAME/KEY: VARIANT
43 <222> LOCATION: (2)..(2)
44 <223> OTHER INFORMATION: Xaa = Val or Ala
46 <220> FEATURE:
47 <221> NAME/KEY: VARIANT
48 <222> LOCATION: (8)..(8)
49 <223> OTHER INFORMATION: Xaa = Asn or Ser
51 <220> FEATURE:
52 <221> NAME/KEY: VARIANT
53 <222> LOCATION: (13)..(13)
54 <223> OTHER INFORMATION: Xaa = Val or Ile
56 <220> FEATURE:
57 <221> NAME/KEY: VARIANT
58 <222> LOCATION: (15)..(15)
59 <223> OTHER INFORMATION: Xaa = Ala or Gly
61 <220> FEATURE:
62 <221> NAME/KEY: VARIANT
```

C--> 13

pg 1-2

Does Not Comply
Corrected Diskette Needed

give source of GRF
(see item 11 on Error
Summary
Sheet)

RAW SEQUENCE LISTING   DATE: 05/01/2006
PATENT APPLICATION: US/10/576,439   TIME: 09:45:10

Input Set : A:\Seq.ST25.txt
Output Set: N:\CRF4\05012006\J576439.raw

```
 63 <222> LOCATION: (18)..(18)
 64 <223> OTHER INFORMATION: Xaa = Ser or Tyr
 66 <220> FEATURE:
 67 <221> NAME/KEY: VARIANT
 68 <222> LOCATION: (24)..(24)
 69 <223> OTHER INFORMATION: Xaa = Gln or His
 71 <220> FEATURE:
 72 <221> NAME/KEY: VARIANT
 73 <222> LOCATION: (25)..(25)
 74 <223> OTHER INFORMATION: Xaa = Asp or Glu
 76 <220> FEATURE:
 77 <221> NAME/KEY: VARIANT
 78 <222> LOCATION: (27)..(27)
 79 <223> OTHER INFORMATION: Xaa = Met or Ile or Nle
 81 <220> FEATURE:
 82 <221> NAME/KEY: VARIANT
 83 <222> LOCATION: (28)..(28)
 84 <223> OTHER INFORMATION: Xaa = Ser or Asn
 86 <220> FEATURE:
 87 <221> NAME/KEY: VARIANT
 88 <222> LOCATION: (30)..(30)
 89 <223> OTHER INFORMATION: Xaa = amino acid sequence of 1 up to 15 residues or is a bond
 91 <400> SEQUENCE: 1
```

W--> 93 Xaa Xaa Asp Ala Ile Phe Tyr Xaa Ser Tyr Arg Lys Xaa Leu Xaa Gln
```
 94 1            5                    10              15
```
W--> 97 Leu Xaa Ala Arg Lys Leu Leu Xaa Xaa Ile Xaa Xaa Arg Xaa
```
 98            20                 25              30
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 44
103 <212> TYPE: PRT
104 <213> ORGANISM: Homo sapiens
107 <220> FEATURE:
108 <221> NAME/KEY: MISC_FEATURE
109 <222> LOCATION: (44)..(44)
110 <223> OTHER INFORMATION: Leu residue is capped with an unsubstituted amide moiety
112 <400> SEQUENCE: 2
114 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
115 1            5                    10              15
118 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
119            20                 25              30
122 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
123            35                 40
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 44
128 <212> TYPE: PRT
129 <213> ORGANISM: Artificial sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Amino acid sequence of human GRF
134 <400> SEQUENCE: 3
```

[Handwritten annotations:] variable length not permitted - see item 5 — on Err summary sheet — Xaa can only represent a single amino acid, nothing else

RAW SEQUENCE LISTING   DATE: 05/01/2006
PATENT APPLICATION: US/10/576,439   TIME: 09:45:10

Input Set : **A:\Seq.ST25.txt**
Output Set: **N:\CRF4\05012006\J576439.raw**

```
136 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
137 1                   5                   10                  15
140 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
141             20                  25                  30
144 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
145         35                  40
148 <210> SEQ ID NO: 4
149 <211> LENGTH: 29
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
154 <220> FEATURE:
155 <221> NAME/KEY: MISC_FEATURE
156 <222> LOCATION: (29)..(29)
157 <223> OTHER INFORMATION: Arg residue is capped with an unsubstituted amide moiety
159 <400> SEQUENCE: 4
161 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
162 1                   5                   10                  15
165 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg
166             20                  25
169 <210> SEQ ID NO: 5
170 <211> LENGTH: 29
171 <212> TYPE: PRT
172 <213> ORGANISM: Artificial sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Amino acid sequence of minimum active core of human GRF
177 <400> SEQUENCE: 5
179 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
180 1                   5                   10                  15
183 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg
184             20                  25
187 <210> SEQ ID NO: 6
188 <211> LENGTH: 15
189 <212> TYPE: PRT
190 <213> ORGANISM: Artificial sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Amino acid sequence corresponding to positions 30 to 44 of human
194      GRF
196 <400> SEQUENCE: 6
198 Gln Gln Gly Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
199 1                   5                   10                  15
202 <210> SEQ ID NO: 7
203 <211> LENGTH: 44
204 <212> TYPE: PRT
205 <213> ORGANISM: Artificial sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Modified GRF peptide
211 <220> FEATURE:
212 <221> NAME/KEY: MISC_FEATURE
213 <222> LOCATION: (1)..(1)
```

RAW SEQUENCE LISTING   DATE: 05/01/2006
PATENT APPLICATION: **US/10/576,439**   TIME: 09:45:10

Input Set : **A:\Seq.ST25.txt**
Output Set: **N:\CRF4\05012006\J576439.raw**

```
214 <223> OTHER INFORMATION: Tyr residue is linked to an hexenoyl-trans-3 moiety
216 <220> FEATURE:
217 <221> NAME/KEY: MISC_FEATURE
218 <222> LOCATION: (44)..(44)
219 <223> OTHER INFORMATION: Leu residue is capped with an unsubstituted amide moiety
221 <400> SEQUENCE: 7
223 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
224 1               5                   10                  15
227 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
228             20                  25                  30
231 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
232         35                  40
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/01/2006
PATENT APPLICATION: **US/10/576,439**   TIME: 09:45:11

Input Set : **A:\Seq.ST25.txt**
Output Set: **N:\CRF4\05012006\J576439.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,8,13,15,18,24,25,27,28,30

VERIFICATION SUMMARY   DATE: 05/01/2006
PATENT APPLICATION: **US/10/576,439**   TIME: 09:45:11

Input Set : **A:\Seq.ST25.txt**
Output Set: **N:\CRF4\05012006\J576439.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16